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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,061

DATE: 09/18/2001

TIME: 16:36:17

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\09182001\I856061.raw

3 <110> APPLICANT: GOITSUKA, Ryo  
 5 <120> TITLE OF INVENTION: A mast cell-specific adapter molecules and cDNAs thereof  
 7 <130> FILE REFERENCE: 2001-0614A/WMC/00653  
 9 <140> CURRENT APPLICATION NUMBER: 09/856,061  
 C--> 10 <141> CURRENT FILING DATE: 2001-07-10  
 12 <150> PRIOR APPLICATION NUMBER: JP11-263778  
 13 <151> PRIOR FILING DATE: 1999-09-17  
 15 <160> NUMBER OF SEQ ID NOS: 4  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1721  
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 22 <213> ORGANISM: Mus musculus  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (255)..(1562)  
 28 <300> PUBLICATION INFORMATION:  
 29 <301> AUTHORS: Goitsuka R., et al.  
 30 <302> TITLE: A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE  
 receptor-

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31 mediated mast cell degranuation  
 32 <303> JOURNAL: Int. Immunol.  
 33 <304> VOLUME: 12  
 34 <305> ISSUE: 4  
 35 <306> PAGES: 573-580  
 36 <307> DATE: 2000-05-26  
 37 <308> DATABASE ACCESSION NO: GenBank/AB021220  
 38 <309> DATABASE ENTRY DATE: 2000-05-26  
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 43 cttacagagt gctccaggat gcgaccgtgg accccctttc caggagctag ccgtctcaac 180  
 44 actgagccct tgactaaagg aagactgagc aggtgagtt gaagatccct ctcttttgcc 240  
 45 aggtgccaaag gacc atg acc agc cag ggc aat aaa agg aca acg aaa gaa 290  
 46 Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu  
 47 1 5 10  
 48 gga ttc ggt gat ctg aga ttc cag aac gtc tct ctg ctg aaa aat agg 338  
 49 Gly Phe Gly Asp Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg  
 50 15 20 25  
 51 tca tgg cca agc ctc agc agt gcc aaa ggg cgg tgt cga gcg gtt ctg 386  
 52 Ser Trp Pro Ser Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu  
 53 30 35 40  
 54 gaa cca ctt ccg gat cac aga agg aac ttg gct ggg gtc cca ggt gga 434  
 55 Glu Pro Leu Pro Asp His Arg Arg Asn Leu Ala Gly Val Pro Gly Gly  
 56 45 50 55 60  
 57 gaa aaa tgc aac agt aac aac gac tac gaa gat cct gag ttc cag ctg 482  
 58 Glu Lys Cys Asn Ser Asn Asn Asp Tyr Glu Asp Pro Glu Phe Gln Leu  
 59 65 70 75

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63 gaa tcg gaa tac gca gat aca cgc tat ttc cag gat atg atg gag gct 578
64 Glu Ser Glu Tyr Ala Asp Thr Arg Tyr Phe Gln Asp Met Met Glu Ala
65 95 100 105
66 ccc ctt ctg tta cct ccc aag gct tct gtc tcc act gag aga caa acc 626
67 Pro Leu Leu Leu Pro Pro Lys Ala Ser Val Ser Thr Glu Arg Gln Thr
68 110 115 120
69 agg gat gtg agg atg aca cag ctg gaa gaa gtg gac aag cct acc ttc 674
70 Arg Asp Val Arg Met Thr Gln Leu Glu Glu Val Asp Lys Pro Thr Phe
71 125 130 135 140
72 aag gat gtc aga agc caa cgc ttt aaa gga ttc aaa tac aca aaa ata 722
73 Lys Asp Val Arg Ser Gln Arg Phe Lys Gly Phe Lys Tyr Thr Lys Ile
74 145 150 155
75 aac aag act cct ttg cca cct cct cgg cct gct atc act ctc ccc aag 770
76 Asn Lys Thr Pro Leu Pro Pro Pro Arg Pro Ala Ile Thr Leu Pro Lys
77 160 165 170
78 aag tac caa ccc tta ccc cca gca cca cca gag gag agc agt gca tac 818
79 Lys Tyr Gln Pro Leu Pro Pro Ala Pro Pro Glu Glu Ser Ser Ala Tyr
80 175 180 185
81 ttc gct cca aag ccc acc ttt cca gaa gtc cag agg ggg ccc agg cag 866
82 Phe Ala Pro Lys Pro Thr Phe Pro Glu Val Gln Arg Gly Pro Arg Gln
83 190 195 200
84 agg agt gca aaa gac ttc agt agg gtc ctt gga gca gaa gaa gaa tct 914
85 Arg Ser Ala Lys Asp Phe Ser Arg Val Leu Gly Ala Glu Glu Glu Ser
86 205 210 215 220
87 cac cac cag aca aag cca gaa tct tct tgc cca tca tca aac caa aac 962
88 His His Gln Thr Lys Pro Glu Ser Ser Cys Pro Ser Ser Asn Gln Asn
89 225 230 235
90 aca cag aag agt cca cct gcc att gcc agc tct tcc tac atg cca gga 1010
91 Thr Gln Lys Ser Pro Pro Ala Ile Ala Ser Ser Ser Tyr Met Pro Gly
92 240 245 250
93 aag cac agt ata caa gcc aga gac cat aca ggt agc atg cag cac tgt 1058
94 Lys His Ser Ile Gln Ala Arg Asp His Thr Gly Ser Met Gln His Cys
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96 cct gct cag aga tgc caa gct gca gcc agc cac agc cct cga atg ctg 1106
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100 Pro Tyr Glu Asn Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp
101 285 290 295 300
102 gag aag gat gtc tgg cag aat gaa tgg tac att gga gaa tac agt cgc 1202
103 Glu Lys Asp Val Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg
104 305 310 315
105 cag gca gtg gaa gat gtg tta atg aaa gag aac aag gat ggt act ttt 1250
106 Gln Ala Val Glu Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe
107 320 325 330
108 ttg gtc cga gac tgc tct aca aaa tcc aag gca gaa cca tat gtt ttg 1298

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113          350          355          360
114 gag agc aat caa cag ttt gcc ctg ggc aca gga cta cga gga aat gag 1394
115 Glu Ser Asn Gln Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu
116 365          370          375          380
117 atg ttt gat tct gtg gaa gac atc att gaa cac tac aca tat ttt ccc 1442
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119          385          390          395
120 att ctg cta ata gat ggg aaa gac aag gct gca cgc agg aaa cag tgc 1490
121 Ile Leu Leu Ile Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys
122          400          405          410
123 tac ctc acc cag cca ctg cct ctc gcc agg ctc ctt ctc act cag tac 1538
124 Tyr Leu Thr Gln Pro Leu Pro Leu Ala Arg Leu Leu Leu Thr Gln Tyr
125          415          420          425
126 tcc agc cag gca ctt cat gag taa gaagcccagc cagatatccc cgcattcagt 1592
127 Ser Ser Gln Ala Leu His Glu
128          430          435
129 gcctgggcct tgtctcattc ctggctcaat ggattcagtt cttcttccat ctgcatttat 1652
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145          35          40          45
146 Asp His Arg Arg Asn Leu Ala Gly Val Pro Gly Gly Glu Lys Cys Asn
147          50          55          60
148 Ser Asn Asn Asp Tyr Glu Asp Pro Glu Phe Gln Leu Leu Lys Ala Trp
149 65          70          75          80
150 Pro Ser Met Lys Ile Leu Pro Ala Arg Pro Ile Gln Glu Ser Glu Tyr
151          85          90          95
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153          100          105          110
154 Pro Pro Lys Ala Ser Val Ser Thr Glu Arg Gln Thr Arg Asp Val Arg
155          115          120          125
156 Met Thr Gln Leu Glu Glu Val Asp Lys Pro Thr Phe Lys Asp Val Arg
157          130          135          140
158 Ser Gln Arg Phe Lys Gly Phe Lys Tyr Thr Lys Ile Asn Lys Thr Pro
159 145          150          155          160
160 Leu Pro Pro Pro Arg Pro Ala Ile Thr Leu Pro Lys Lys Tyr Gln Pro

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164 Pro Thr Phe Pro Glu Val Gln Arg Gly Pro Arg Gln Arg Ser Ala Lys
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167 210 215 220
168 Lys Pro Glu Ser Ser Cys Pro Ser Ser Asn Gln Asn Thr Gln Lys Ser
169 225 230 235 240
170 Pro Pro Ala Ile Ala Ser Ser Ser Tyr Met Pro Gly Lys His Ser Ile
171 245 250 255
172 Gln Ala Arg Asp His Thr Gly Ser Met Gln His Cys Pro Ala Gln Arg
173 260 265 270
174 Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu Pro Tyr Glu Asn
175 275 280 285
176 Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp Glu Lys Asp Val
177 290 295 300
178 Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu
179 305 310 315 320
180 Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe Leu Val Arg Asp
181 325 330 335
182 Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu Val Val Phe Tyr
183 340 345 350
184 Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Ser Asn Gln
185 355 360 365
186 Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu Met Phe Asp Ser
187 370 375 380
188 Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro Ile Leu Leu Ile
189 385 390 395 400
190 Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys Tyr Leu Thr Gln
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203 <220> FEATURE:
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205 <222> LOCATION: (1)..(1128)
207 <300> PUBLICATION INFORMATION:
208 <301> AUTHORS: Goitsuka R., et al.
209 <302> TITLE: A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE
receptor-
210 mediated mast cell degranuation
211 <303> JOURNAL: Int. Immunol.
212 <304> VOLUME: 12
213 <305> ISSUE: 4

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224 Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp Trp
225 20 25 30
226 gaa aga aac ttt gct gca gtc ctg gat gga gca aaa ggc cac agt gat 144
227 Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His Ser Asp
228 35 40 45
229 gat gac tat gat gac cct gag ctt cgg atg gaa gag aca tgg cag tcg 192
230 Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln Ser
231 50 55 60
232 att aaa att tta cca gcc cgg cct ata aag gaa tct gaa tat gca gat 240
233 Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala Asp
234 65 70 75 80
235 aca cac tat ttc aag gtt gca atg gac act ccc ctt ccg tta gac acc 288
236 Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp Thr
237 85 90 95
238 agg acc tct atc tcc att gga cag ccg acc tgg aac aca cag acg agg 336
239 Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr Arg
240 100 105 110
241 ttg gaa aga gtg gac aaa ccc att tcc agg gac gtc aga agc caa aac 384
242 Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser Gln Asn
243 115 120 125
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246 130 135 140
247 cct cgg cct ctc ata aca ctt ccg aag aag tac caa ccc ttg ccc cct 480
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258 195 200 205
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260 Thr His Leu Leu Glu Asn Gln Asn Thr Gln Glu Ile Pro Leu Ala Ile
261 210 215 220
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VERIFICATION SUMMARY

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